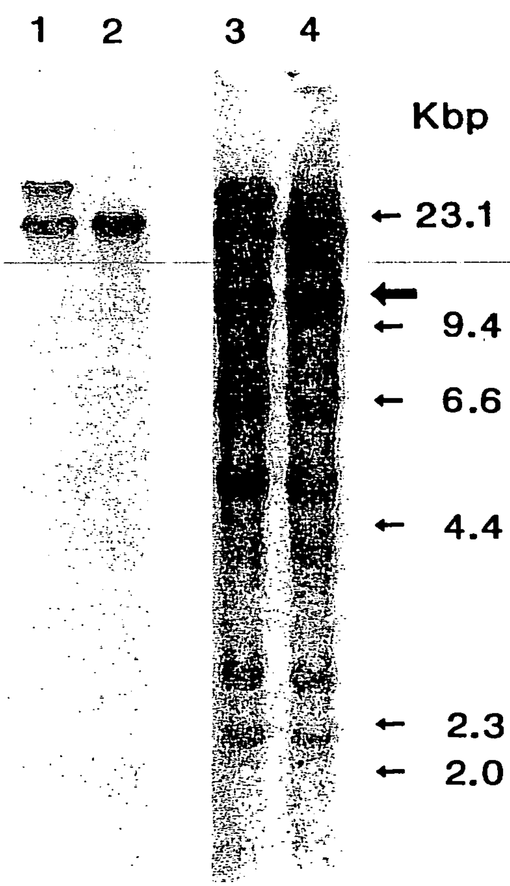


FIG.1A

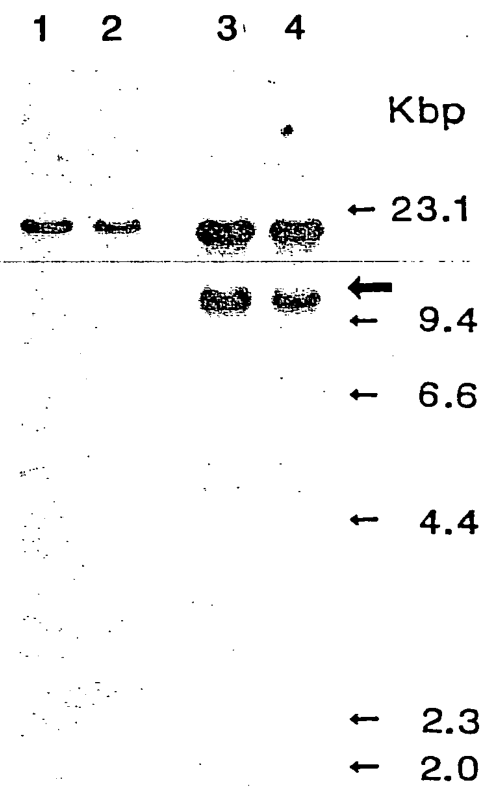


FIG.1B

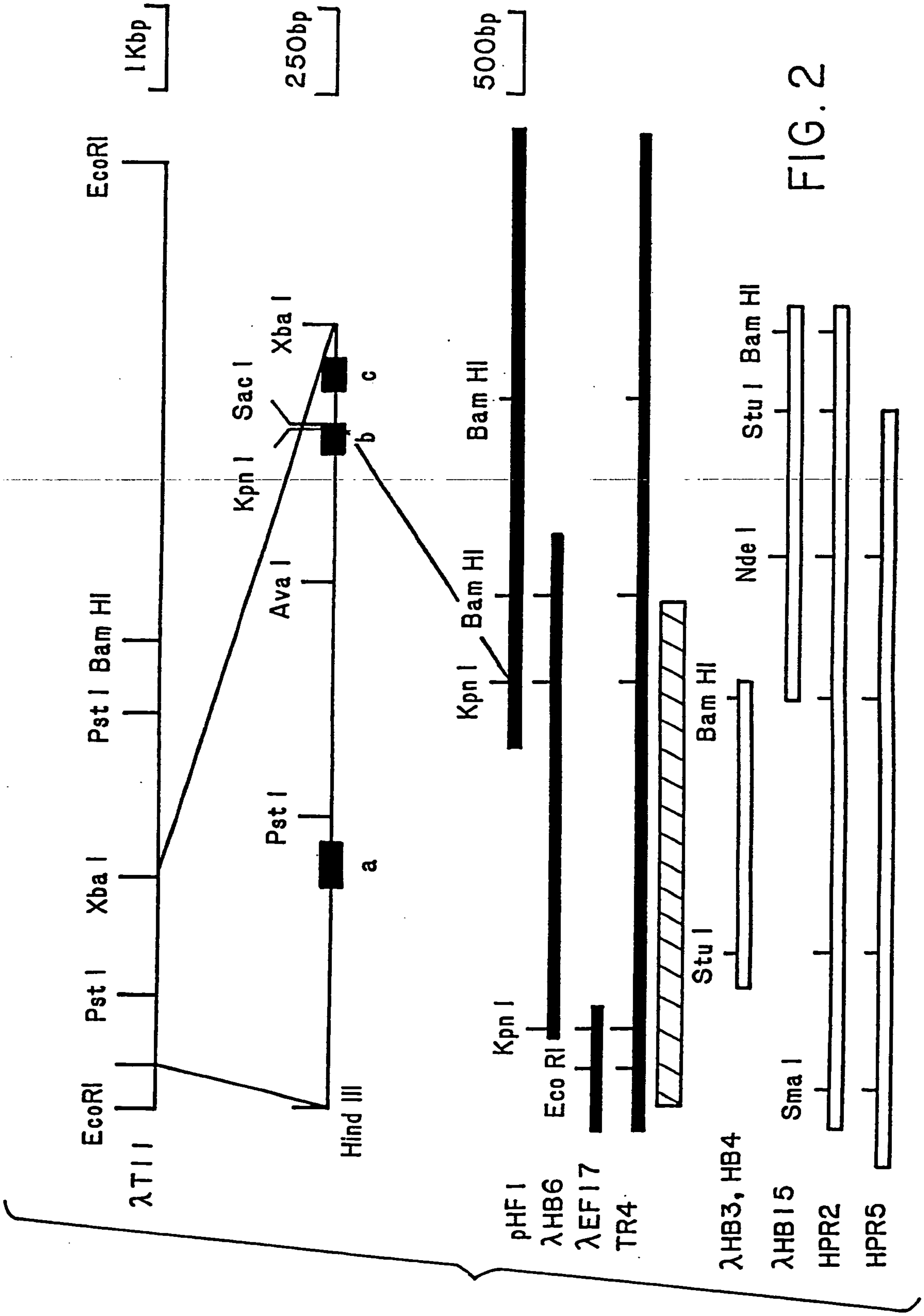

1Kbp
250bp
500bp
EcoRI
Pst I
Xba I
Pst I
Bam HI
EcoRI
Hind III
Pst I
a
Ava I
Kpn I
Sac I
Xba I
b
c
Kpn I
Bam HI
Bam HI
Kpn I
Eco RI
Stu I
Bam HI
Nde I
Stu I
Bam HI
Sma I
λT11
pHF1
λHB6
λEF17
TR4
λHB3, HB4
λHB15
HPR2
HPR5

FIG. 2

FIG. 3-1

```
  1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGA

 49 TCATTTGGGAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATT

                                                MetGly
100 CATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTATGGGG

           5                 10                 15
    ThrSerHisProAlaPheLeuValLeuGlyCysLeuLeuThrGly
145 ACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGG

          20                 25                 30
    LeuSerLeuIleLeuCysGlnLeuSerLeuProSerIleLeuPro
190 CTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCA

          35                 40                 45
    AsnGluAsnGluLysValValGlnLeuAsnSerSerPheSerLeu
235 AATGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTG

          50                 55                 60
    ArgCysPheGlyGluSerGluValSerTrpGlnTyrProMetSer
280 AGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCCATGTCT

          65                 70                 75
    GluGluGluSerSerAspValGluIleArgAsnGluGluAsnAsn
325 GAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAAC

          80                 85                 90
    SerGlyLeuPheValThrValLeuGluValSerSerAlaSerAla
370 AGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCG

          95                100                105
    AlaHisThrGlyLeuTyrThrCysTyrTyrAsnHisThrGlnThr
415 GCCCACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACA

         110                115                120
    GluGluAsnGluLeuGluGlyArgHisIleTyrIleTyrValPro
460 GAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTATGTGCCA

         125                130                135
    AspProAspValAlaPheValProLeuGlyMetThrAspTyrLeu
505 GACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTA
```

FIG. 3-2

```
          140                 145                 150
     ValIleValGluAspAspAspSerAlaIleIleProCysArgThr
 550 GTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACA

          155                 160                 165
     ThrAspProGluThrProValThrLeuHisAsnSerGluGlyVal
 595 ACTGATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTG

          170                 175                 180
     ValProAlaSerTyrAspSerArgGlnGlyPheAsnGlyThrPhe
 640 GTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGACCTTC

          185                 190                 195
     ThrValGlyProTyrIleCysGluAlaThrValLysGlyLysLys
 685 ACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAG

          200                 205                 210
     PheGlnThrIleProPheAsnValTyrAlaLeuLysAlaThrSer
 730 TTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCA

          215                 220                 225
     GluLeuAspLeuGluMetGluAlaLeuLysThrValTyrLysSer
 775 GAGCTGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCA

          230                 235                 240
     GlyGluThrIleValValThrCysAlaValPheAsnAsnGluVal
 820 GGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAATGAGGTG

          245                 250                 255
     ValAspLeuGlnTrpThrTyrProGlyGluValLysGlyLysGly
 865 GTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGC

          260                 265                 270
     IleThrMetLeuGluGluIleLysValProSerIleLysLeuVal
 910 ATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTG

          275                 280                 285
     TyrThrLeuThrValProGluAlaThrValLysAspSerGlyAsp
 955 TACACTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGAT

          290                 295                 300
     TyrGluCysAlaAlaArgGlnAlaThrArgGluValLysGluMet
1000 TACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAAGAAATG

          305                 310                 315
     LysLysValThrIleSerValHisGluLysGlyPheIleGluIle
1045 AAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATC
```

FIG. 3-3

```
          320                  325                  330
     LysProThrPheSerGlnLeuGluAlaValAsnLeuHisGluVal
1090 AAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTC

          335                  340                  345
     LysHisPheValValGluValArgAlaTyrProProProArgIle
1135 AAACATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATA

          350                  355                  360
     SerTrpLeuLysAsnAsnLeuThrLeuIleGluAsnLeuThrGlu
1180 TCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTCACTGAG

          365                  370                  375
     IleThrThrAspValGluLysIleGlnGluIleArgTyrArgSer
1225 ATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGC

          380                  385                  390
     LysLeuLysLeuIleArgAlaLysGluGluAspSerGlyHisTyr
1270 AAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTAT

          395                  400                  405
     ThrIleValAlaGlnAsnGluAspAlaValLysSerTyrThrPhe
1315 ACTATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTT

          410                  415                  420
     GluLeuLeuThrGlnValProSerSerIleLeuAspLeuValAsp
1360 GAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTGGTCGAT

          425                  430                  435
     AspHisHisGlySerThrGlyGlyGlnThrValArgCysThrAla
1405 GATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCT

          440                  445                  450
     GluGlyThrProLeuProAspIleGluTrpMetIleCysLysAsp
1450 GAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGAT

          455                  460                  465
     IleLysLysCysAsnAsnGluThrSerTrpThrIleLeuAlaAsn
1495 ATTAAGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAAC

          470                  475                  480
     AsnValSerAsnIleIleThrGluIleHisSerArgAspArgSer
1540 AATGTCTCAAACATCATCACGGAGATCCACTCCCGAGACAGGAGT

          485                  490                  495
     ThrValGluGlyArgValThrPheAlaLysValGluGluThrIle
1585 ACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATC
```

FIG. 3-4

```
            500            505            510
     AlaValArgCysLeuAlaLysAsnLeuLeuGlyAlaGluAsnArg
1630 GCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGA

            515            520            525
     GluLeuLysLeuValAlaProThrLeuArgSerGluLeuThrVal
1675 GAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTG

            530            535            540
     AlaAlaAlaValLeuValLeuLeuValIleValIleIleSerLeu
1720 GCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTT

            545            550            555
     IleValLeuValValIleTrpLysGlnLysProArgTyrGluIle
1765 ATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATT

            560            565            570
     ArgTrpArgValIleGluSerIleSerProAspGlyHisGluTyr
1810 CGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATAT

            575            580            585
     IleTyrValAspProMetGlnLeuProTyrAspSerArgTrpGlu
1855 ATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAG

            590            595            600
     PheProArgAspGlyLeuValLeuGlyArgValLeuGlySerGly
1900 TTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGA

            605            610            615
     AlaPheGlyLysValValGluGlyThrAlaTyrGlyLeuSerArg
1945 GCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGG

            620            625            630
     SerGlnProValMetLysValAlaValLysMetLeuLysProThr
1990 TCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACG

            635            640            645
     AlaArgSerSerGluLysGlnAlaLeuMetSerGluLeuLysIle
2035 GCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATA

            650            655            660
     MetThrHisLeuGlyProHisLeuAsnIleValAsnLeuLeuGly
2080 ATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGA

            665            670            675
     AlaCysThrLysSerGlyProIleTyrIleIleThrGluTyrCys
2125 GCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGC
```

FIG. 3-5

```
      680                 685                 690
     PheTyrGlyAspLeuValAsnTyrLeuHisLysAsnArgAspSer
2170 TTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGC

      695                 700                 705
     PheLeuSerHisHisProGluLysProLysLysGluLeuAspIle
2215 TTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATC

      710                 715                 720
     PheGlyLeuAsnProAlaAspGluSerThrArgSerTyrValIle
2260 TTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATT

      725                 730                 735
     LeuSerPheGluAsnAsnGlyAspTyrMetAspMetLysGlnAla
2305 TTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCT

      740                 745                 750
     AspThrThrGlnTyrValProMetLeuGluArgLysGluValSer
2350 GATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCT

      755                 760                 765
     LysTyrSerAspIleGlnArgSerLeuTyrAspArgProAlaSer
2395 AAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCA

      770                 775                 780
     TyrLysLysLysSerMetLeuAspSerGluValLysAsnLeuLeu
2440 TATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTT

      785                 790                 795
     SerAspAspAsnSerGluGlyLeuThrLeuLeuAspLeuLeuSer
2485 TCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGC

      800                 805                 810
     PheThrTyrGlnValAlaArgGlyMetGluPheLeuAlaSerLys
2530 TTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAA

      815                 820                 825
     AsnCysValHisArgAspLeuAlaAlaArgAsnValLeuLeuAla
2575 AATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCA

      830                 835                 840
     GlnGlyLysIleValLysIleCysAspPheGlyLeuAlaArgAsp
2620 CAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGAC

      845                 850                 855
     IleMetHisAspSerAsnTyrValSerLysGlySerThrPheLeu
2665 ATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTG
```

FIG. 3-6

860 865 870
ProValLysTrpMetAlaProGluSerIlePheAspAsnLeuTyr
2710 CCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTAC
a

875 880 885
ThrThrLeuSerAspValTrpSerTyrGlyIleLeuLeuTrpGlu
2755 ACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAG

890 895 900
IlePheSerLeuGlyGlyThrProTyrProGlyMetMetValAsp
2800 ATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGAT

905 910 915
SerThrPheTyrAsnLysIleLysSerGlyTyrArgMetAlaLys
2845 TCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAG
b

920 925 930
ProAspHisAlaThrSerGluValTyrGluIleMetValLysCys
2890 CCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGC

935 940 945
TrpAsnSerGluProGluLysArgProSerPheTyrHisLeuSer
2935 TGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGT
c

950 955 960
GluIleValGluAsnLeuLeuProGlyGlnTyrLysLysSerTyr
2980 GAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTAT

965 970 975
GluLysIleHisLeuAspPheLeuLysSerAspHisProAlaVal
3025 GAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTG

980 985 990
AlaArgMetArgValAspSerAspAsnAlaTyrIleGlyValThr
3070 GCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACC

995 1000 1005
TyrLysAsnGluGluAspLysLeuLysAspTrpGluGlyGlyLeu
3115 TACAAAAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTG

FIG. 3-7

```
             1010                1015                1020
     AspGluGlnArgLeuSerAlaAspSerGlyTyrIleIleProLeu
3160 GATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTCTG

             1025                1030                1035
     ProAspIleAspProValProGluGluGluAspLeuGlyLysArg
3205 CCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGG

             1040                1045                1050
     AsnArgHisSerSerGlnThrSerGluGluSerAlaIleGluThr
3250 AACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACG

             1055                1060                1065
     GlySerSerSerSerThrPheIleLysArgGluAspGluThrIle
3295 GGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATT

             1070                1075                1080
     GluAspIleAspMetMetAspAspIleGlyIleAspSerSerAsp
3340 GAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAGAC

             1085
     LeuValGluAspSerPheLeu
3385 CTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCC

3430 TTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTT

3475 TATTGCAATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAA

3520 GAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAATATGAA

3565 TGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGC

3610 AATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGA

3655 TGGATAAGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCA

3700 AGGACATTGGTGAGAGTCCAACAGACACAATTTATACTGCGACAG

3745 AACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTG

3790 TTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCAC

3835 TCAATCCATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGC

3880 TGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTTGAACCT

3925 TAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTT
```

FIG. 3-8

3970 AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTG

4015 GGTCATTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATG

4060 TTTATAATACTACTACTGTTATCAGTAATGCTAAATGTGTAATAA

4105 TGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCC

4150 TTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTA

4195 AATAACATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATT

4240 AAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTGTTGTCCA

4285 GGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCAT

4330 CGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGA

4375 AACAAACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCA

4420 TAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAATGGA

4465 AAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTT

4510 TTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATAT

4555 GTATTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCC

4600 AGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAAGAG

4645 TTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGAT

4690 GTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCA

4735 GGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATG

4780 AAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGC

4825 TGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGG

4870 AAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTG

4915 GAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCA

4960 GGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAA

5005 TTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGG

FIG. 3-9

5050 TTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTAT

5095 GGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACT

5140 CCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCA

5185 GTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAA

5230 AACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATG

5275 AATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTC

5320 ATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAA

5365 TGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGA

5410 TGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTAC

5455 CTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACT

5500 TTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAA

5545 ACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATA

5590 CGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCT

5635 CACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTG

5680 ATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACT

5725 TCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAA

5770 TTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAA

5815 TTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGA

5860 AAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCA

5905 AAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGT

5950 GATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTA

5995 TTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAAT

6040 ATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAA

6085 CATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAA

```
6130   CTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATG
6175   TCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACA
6220   TGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACT
6265   TGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTC
6310   ATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAA
6355   TAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAA
6400   AAAAAAAAAAAAAA
```

FIG. 3-10

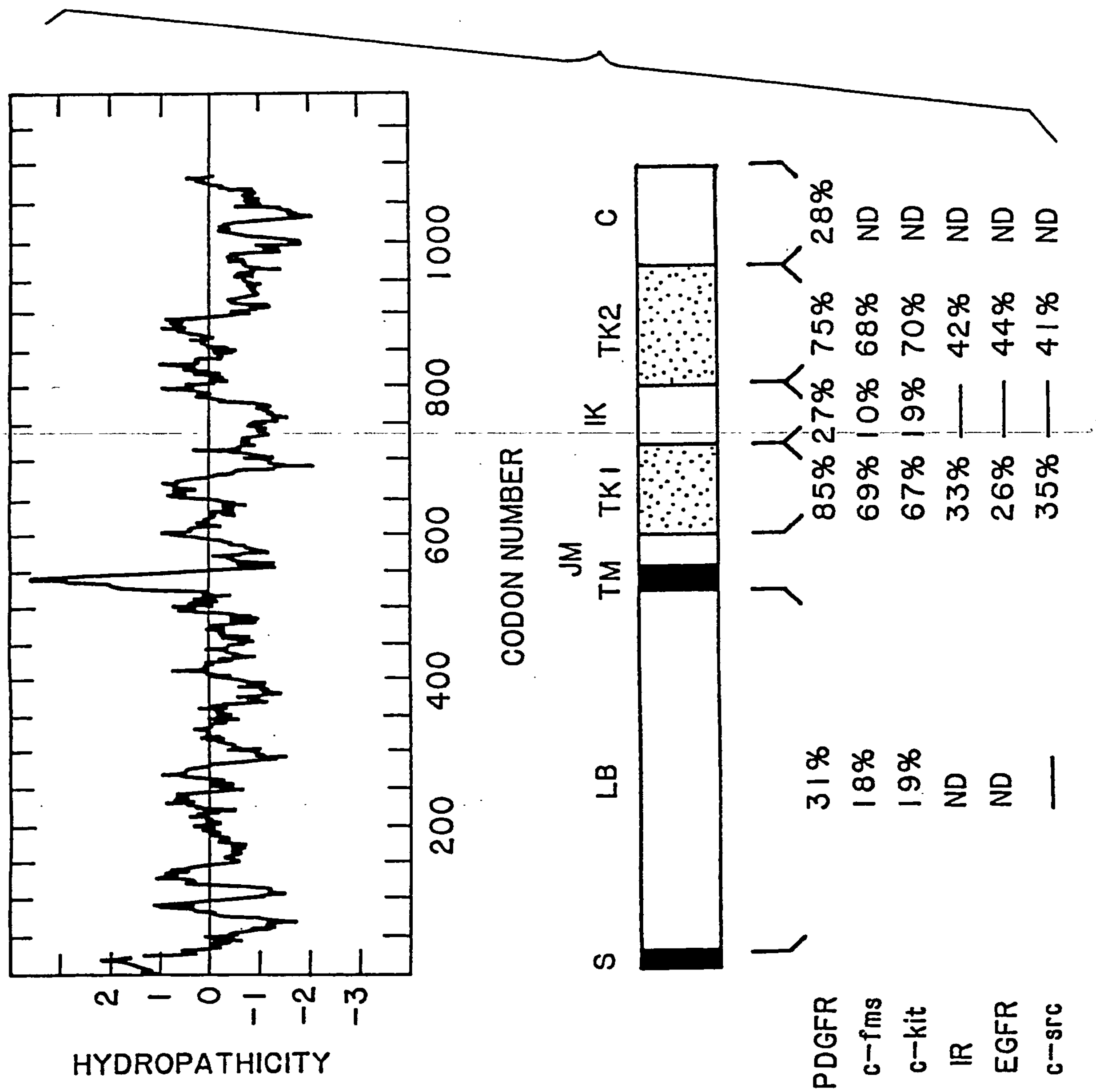
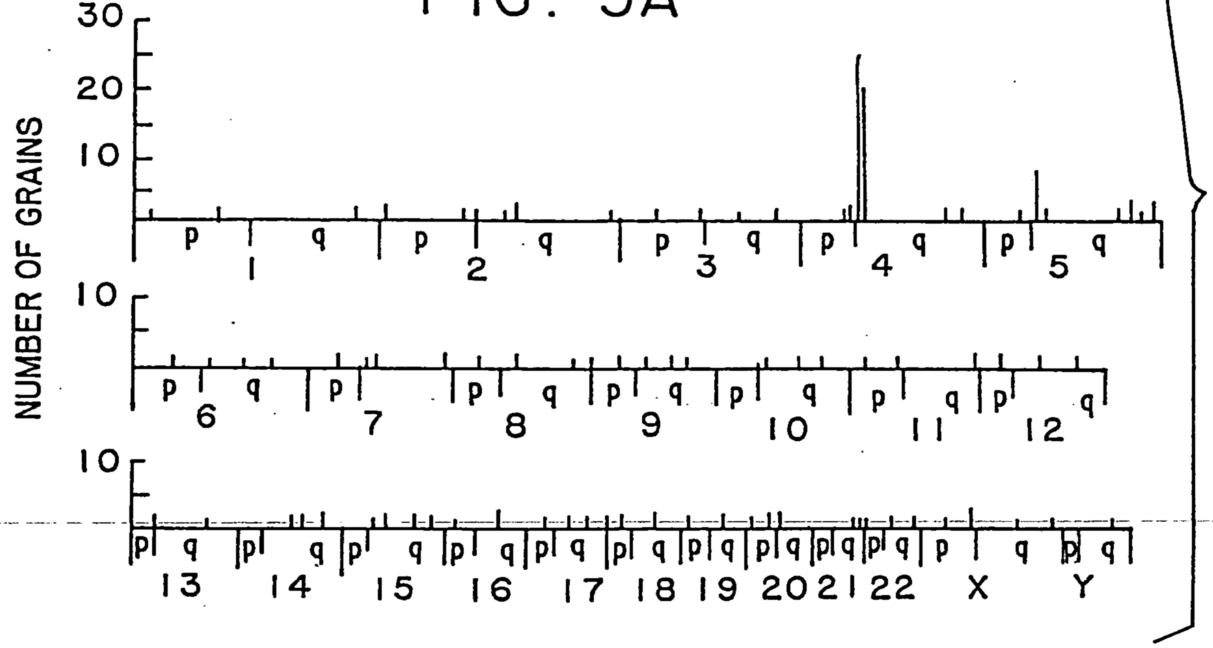

HYDROPATHICITY
2
1
0
-1
-2
-3
200
400
600
800
1000
CODON NUMBER
S
LB
TM
JM
TK1
IK
TK2
C
PDGFR 31% 85% 27% 75% 28%
c-fms 18% 69% 10% 68% ND
c-kit 19% 67% 19% 70% ND
IR ND 33% — 42% ND
EGFR ND 26% — 44% ND
c-src — 35% — 41% ND

FIG. 4

FIG. 5A


NUMBER OF GRAINS
30
20
10
p q 1 p 2 q p 3 q p 4 q p 5 q
10
p 6 q p 7 p 8 q p 9 q p 10 q p 11 q p 12 q
10
p 13 q p 14 q p 15 q p 16 q p 17 q p 18 q p 19 q p 20 q p 21 q p 22 q p X q p Y q

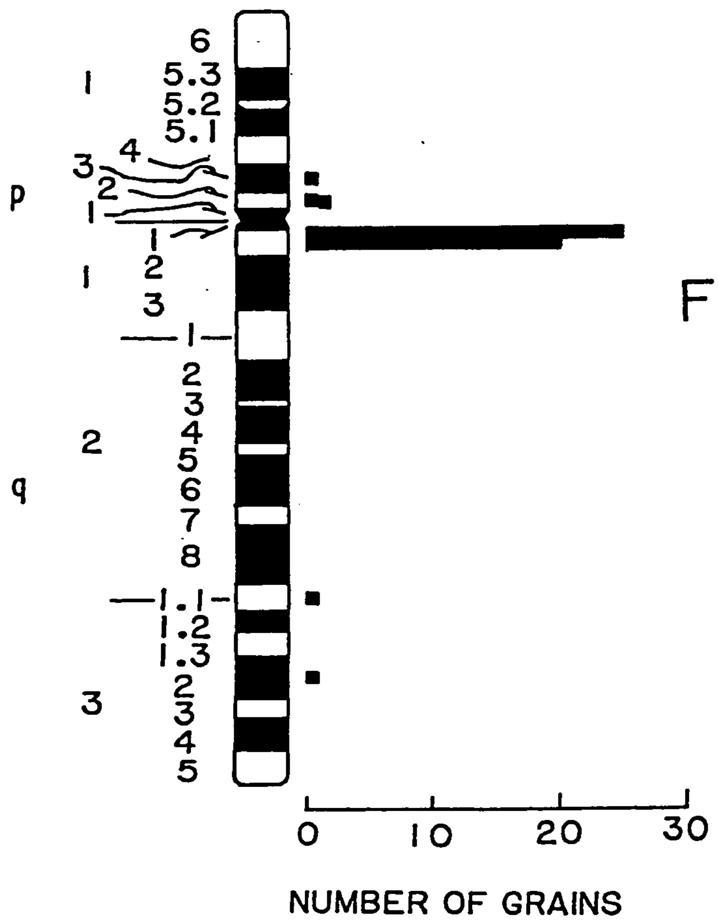

p
q
6
5.3
5.2
5.1
4
3
2
1
1
2
3
1
2
3
4
5
6
7
8
1.1
1.2
1.3
2
3
4
5
0
10
20
30
NUMBER OF GRAINS

FIG. 5B

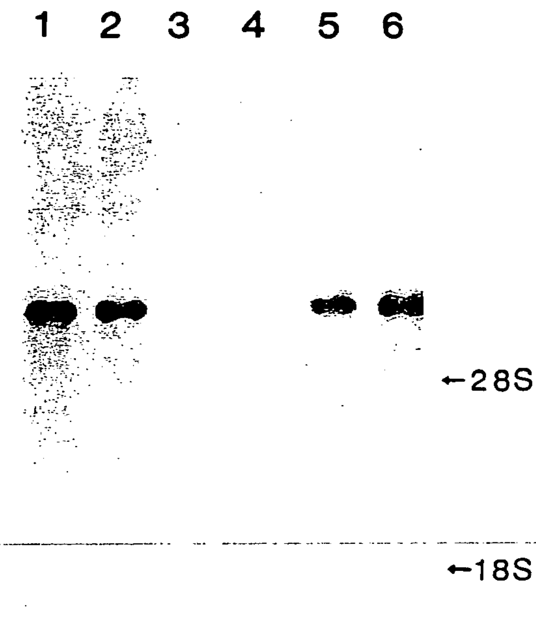


FIG.6A

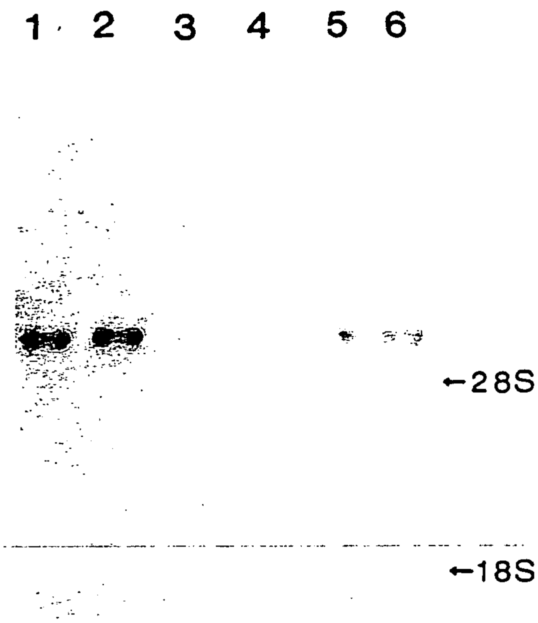


FIG.6B

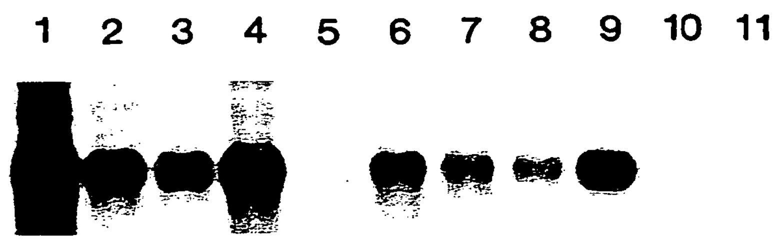


FIG.6C

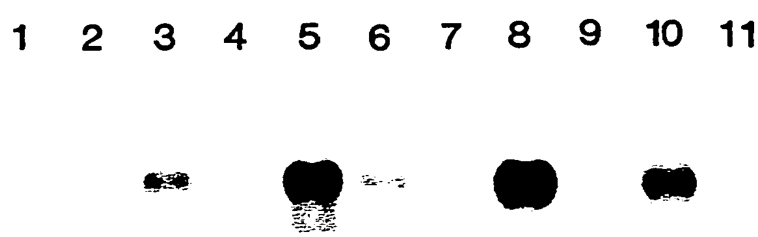


FIG.6D

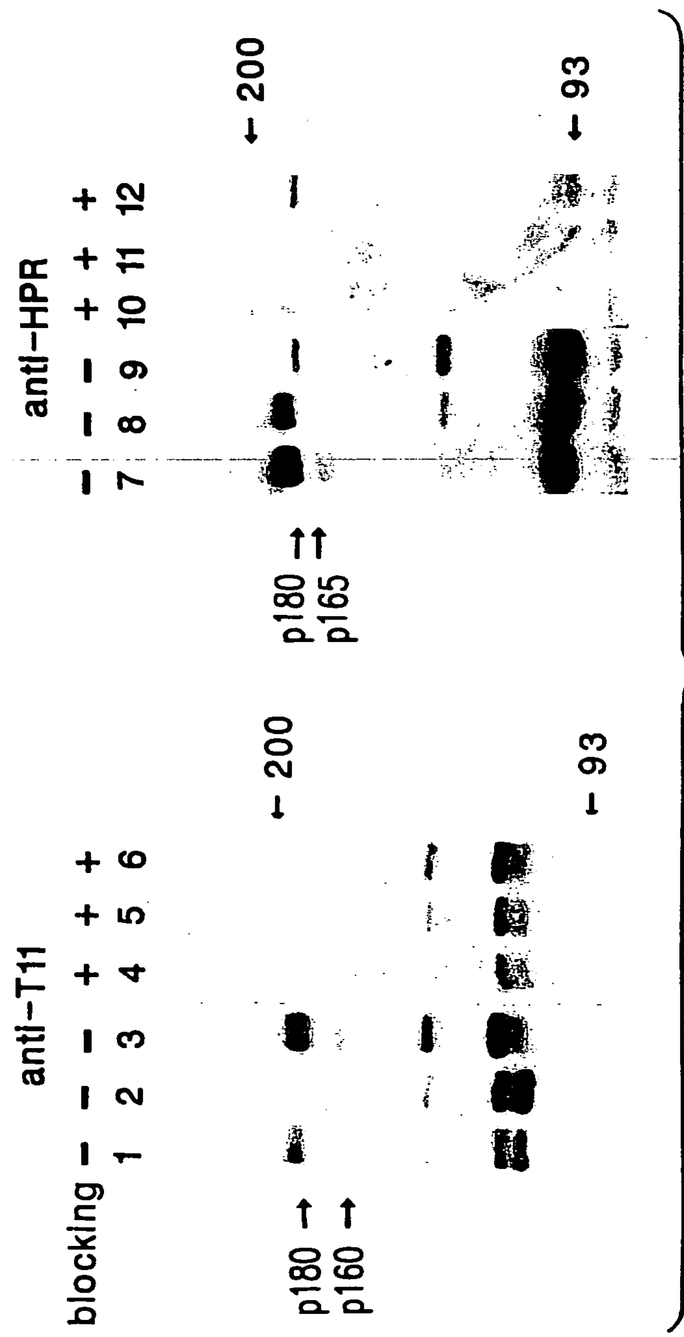

anti-T11
anti-HPR
blocking – – – + + + – – – + + +
1 2 3 4 5 6 7 8 9 10 11 12
200
93
200
93
p180
p160
p180
p165

FIG.7A

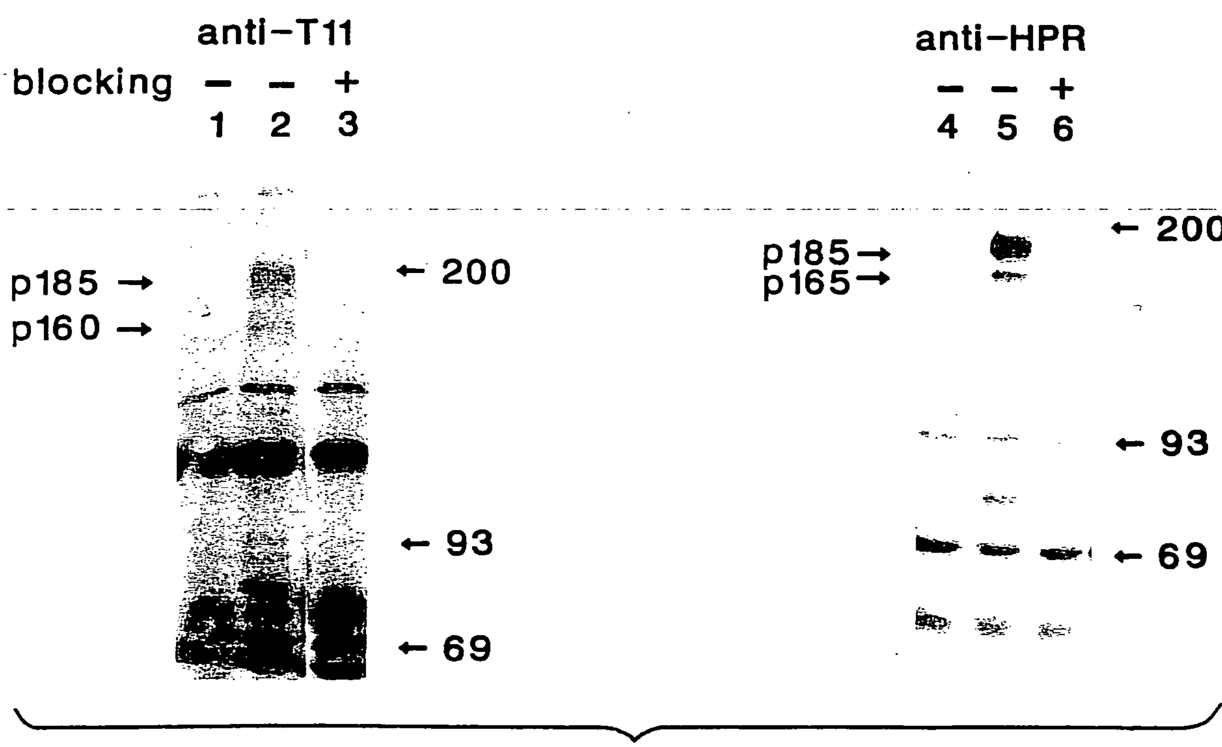

anti-T11
blocking
− − +
1 2 3
p185 →
p160 →
← 200
← 93
← 69
anti-HPR
− − +
4 5 6
p185→
p165→
← 200
← 93
← 69

FIG.7B

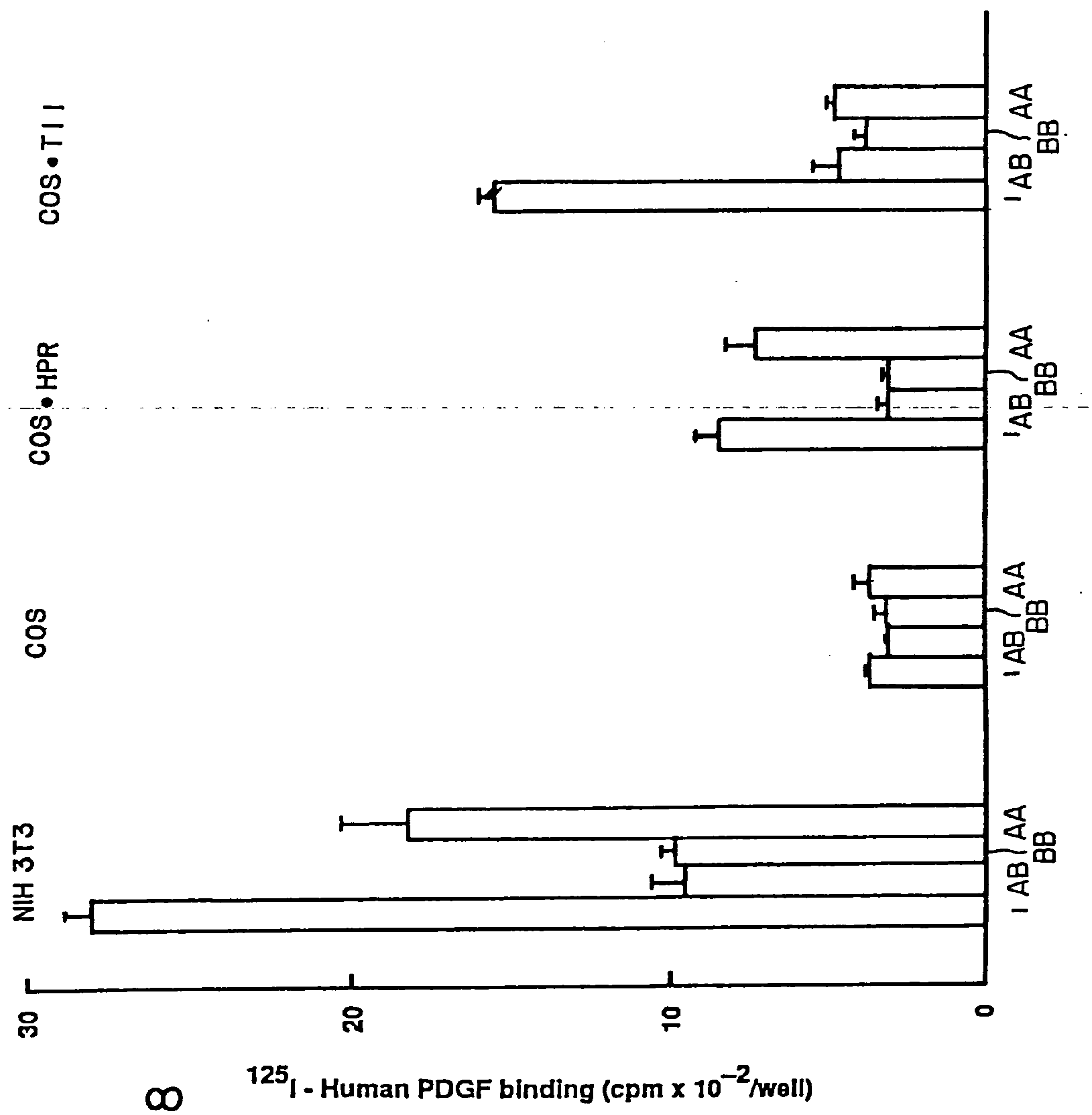

NIH 3T3
COS
COS • HPR
COS • T11
I
AB
BB
AA
30
20
10
0
125I - Human PDGF binding (cpm x 10−2/well)

FIG. 8

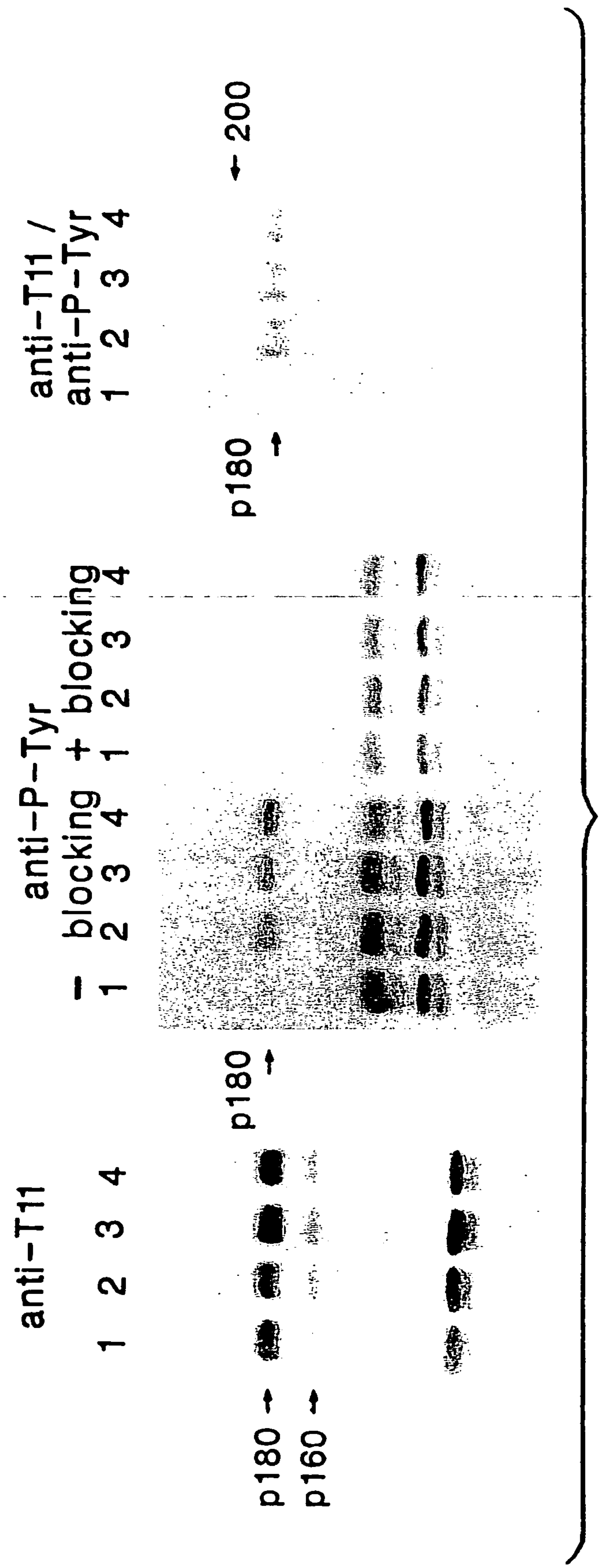

anti-T11
1 2 3 4
p180
p160
anti-P-Tyr
- blocking
1 2 3 4
+ blocking
1 2 3 4
p180
anti-T11 /
anti-P-Tyr
1 2 3 4
p180
200

FIG.9A

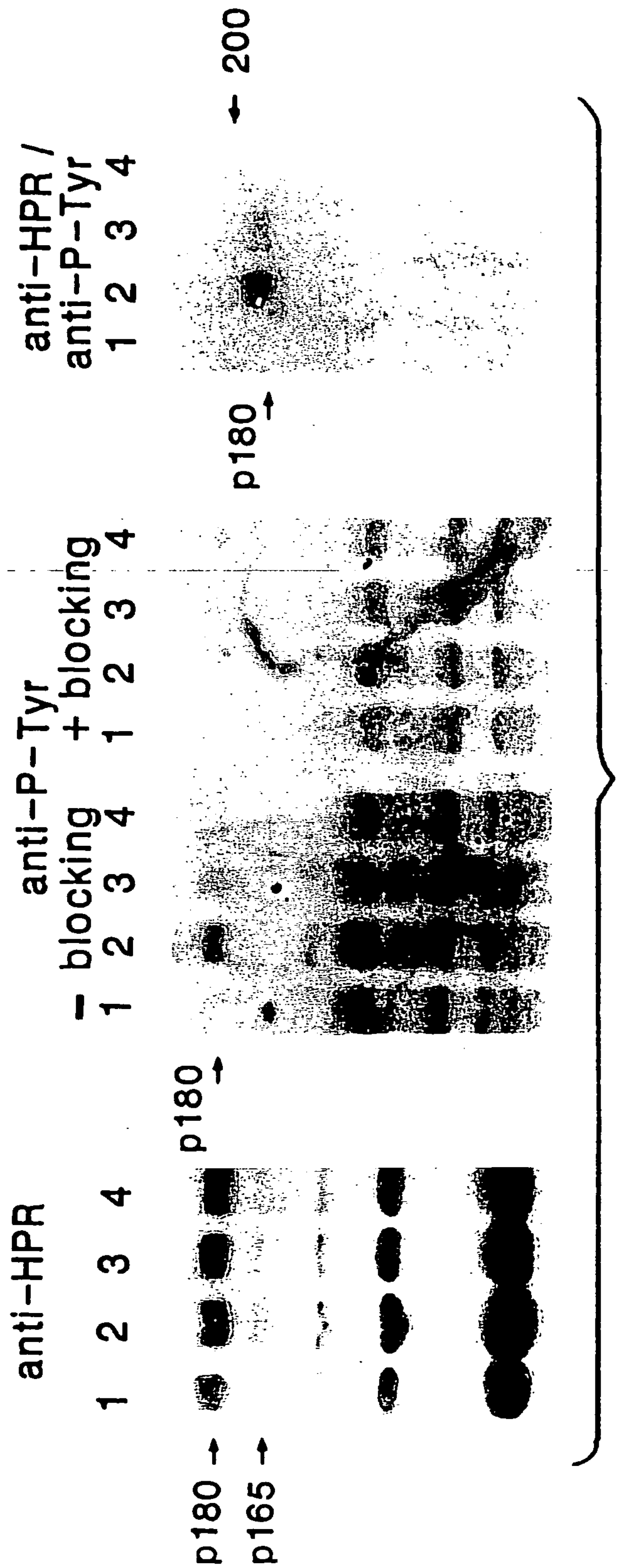
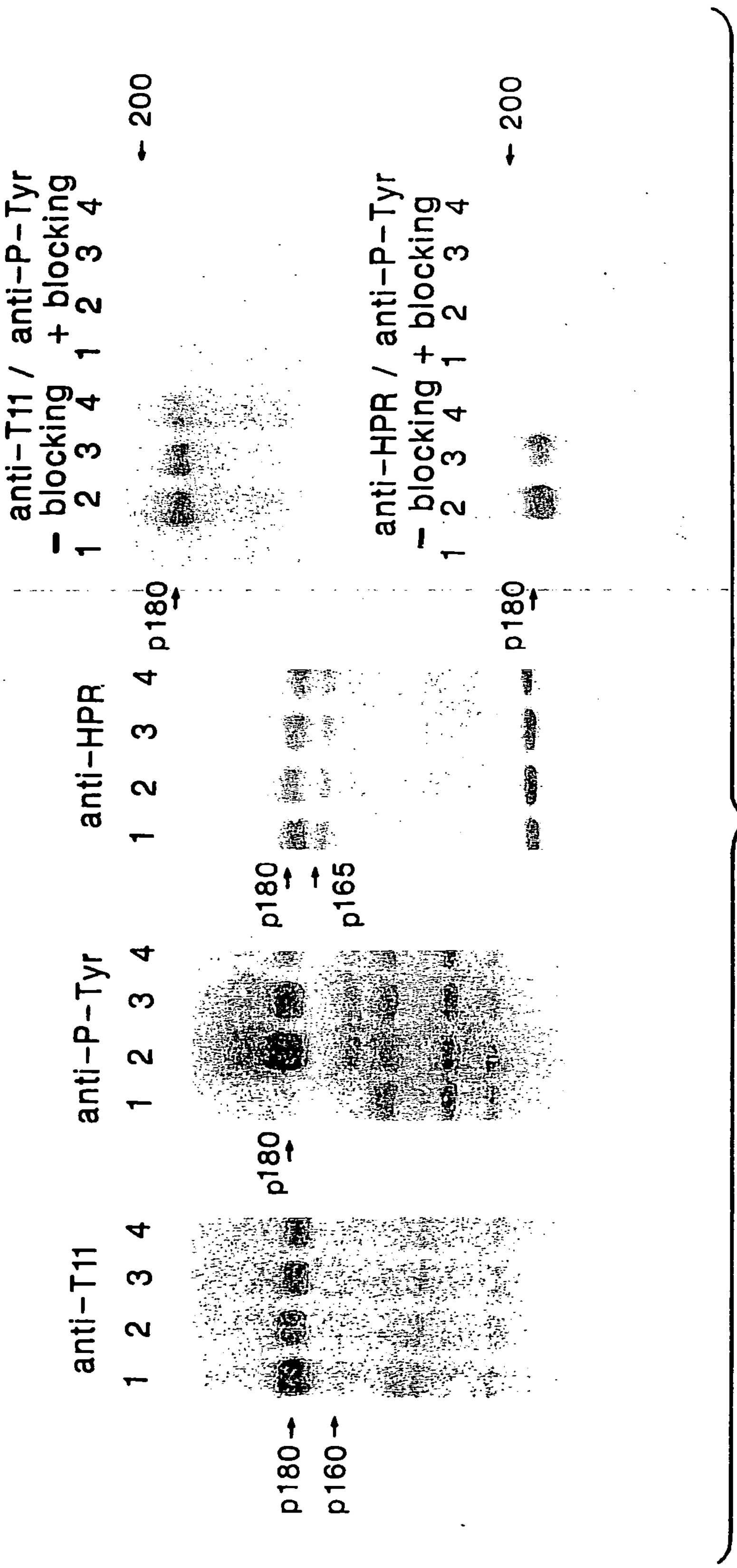

anti-HPR
1 2 3 4
p180
p165
anti-P-Tyr
− blocking
1 2 3 4
+ blocking
1 2 3 4
anti-HPR /
anti-P-Tyr
1 2 3 4
200

FIG.9B



anti-T11 / anti-P-Tyr
− blocking + blocking
1 2 3 4 1 2 3 4
← 200
p180
anti-HPR / anti-P-Tyr
− blocking + blocking
1 2 3 4 1 2 3 4
← 200
p180
anti-HPR
1 2 3 4
p180
p165
anti-P-Tyr
1 2 3 4
p180
anti-T11
1 2 3 4
p180
p160

FIG.9C

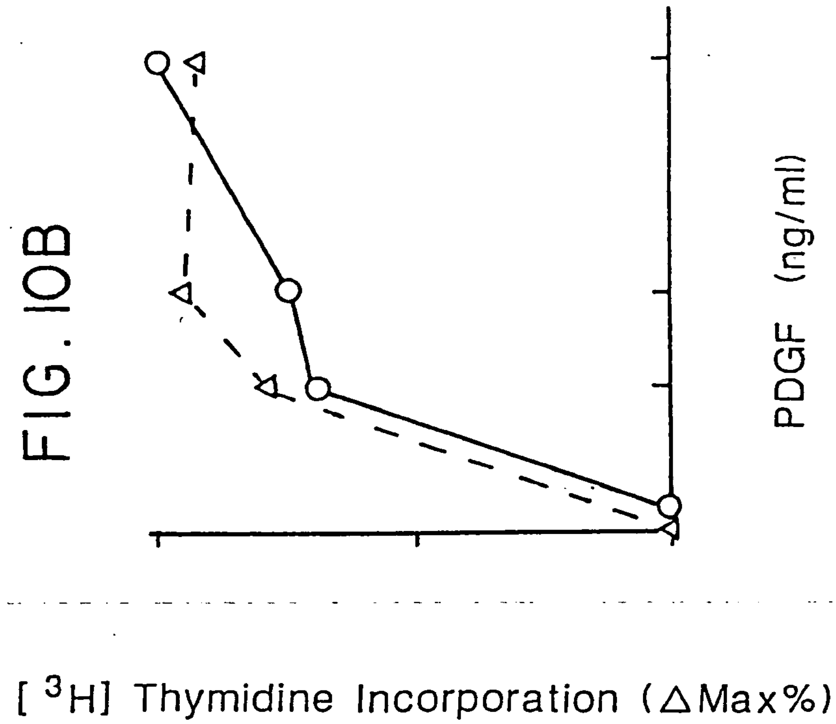


FIG. 10B

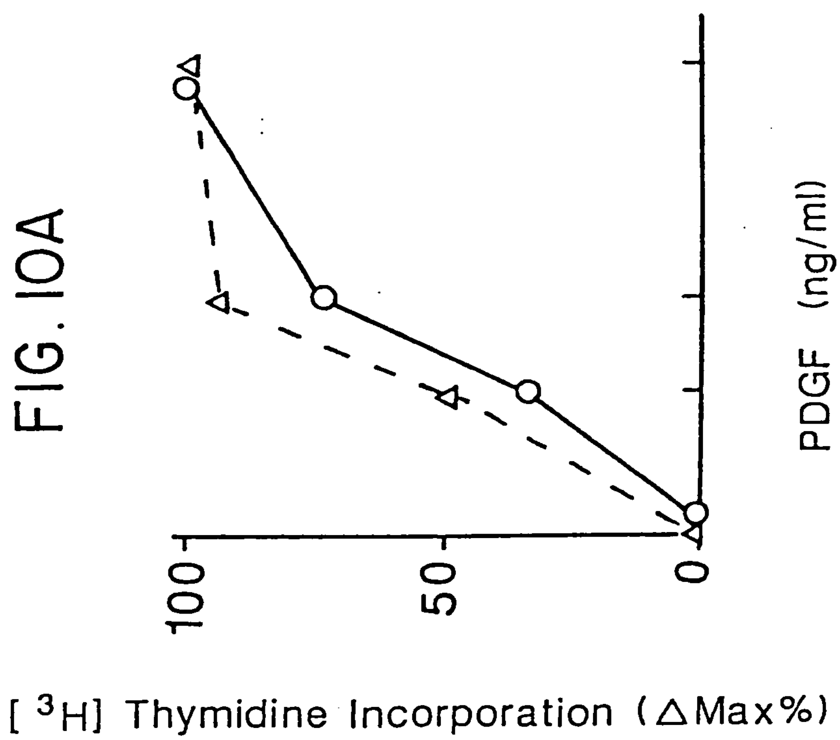


FIG. 10A

FIG. 10D

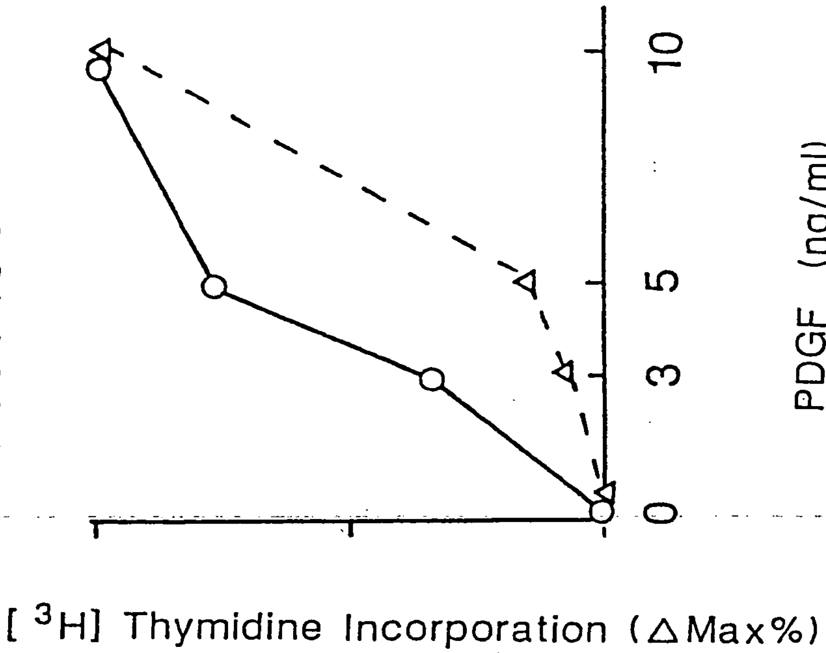
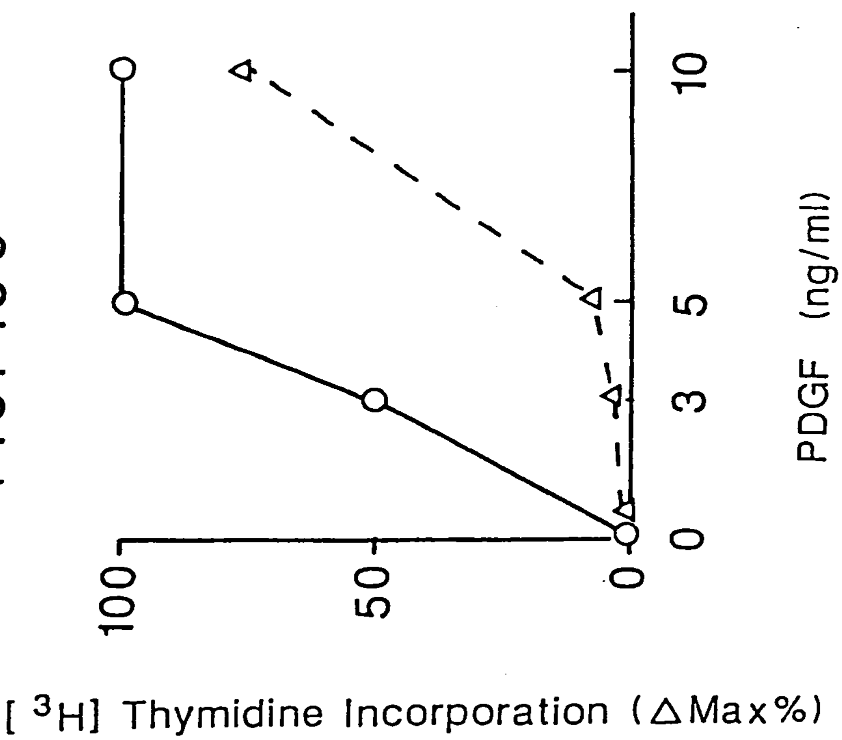


FIG. 10C



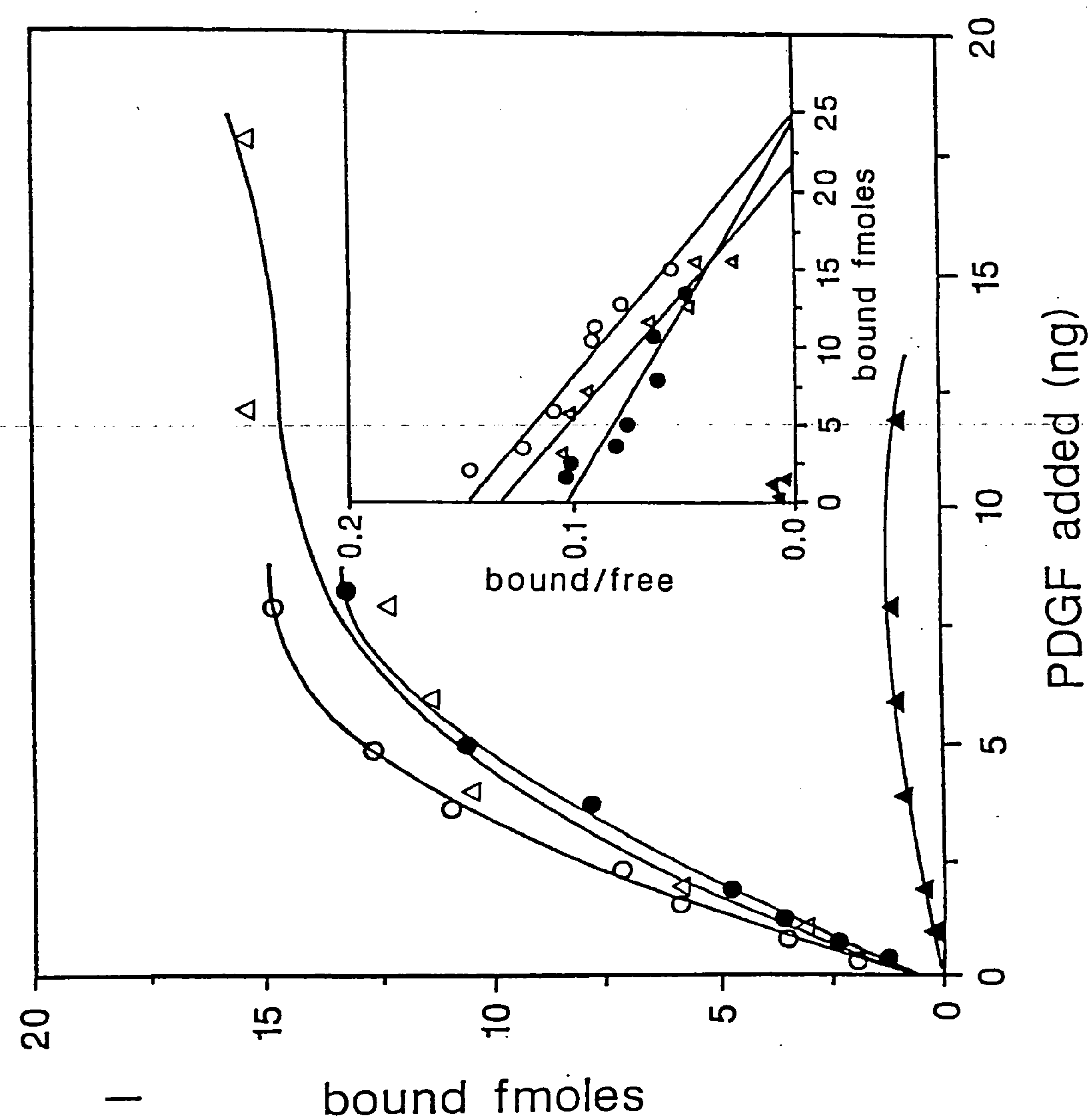


FIG. 11

FIG. 12A

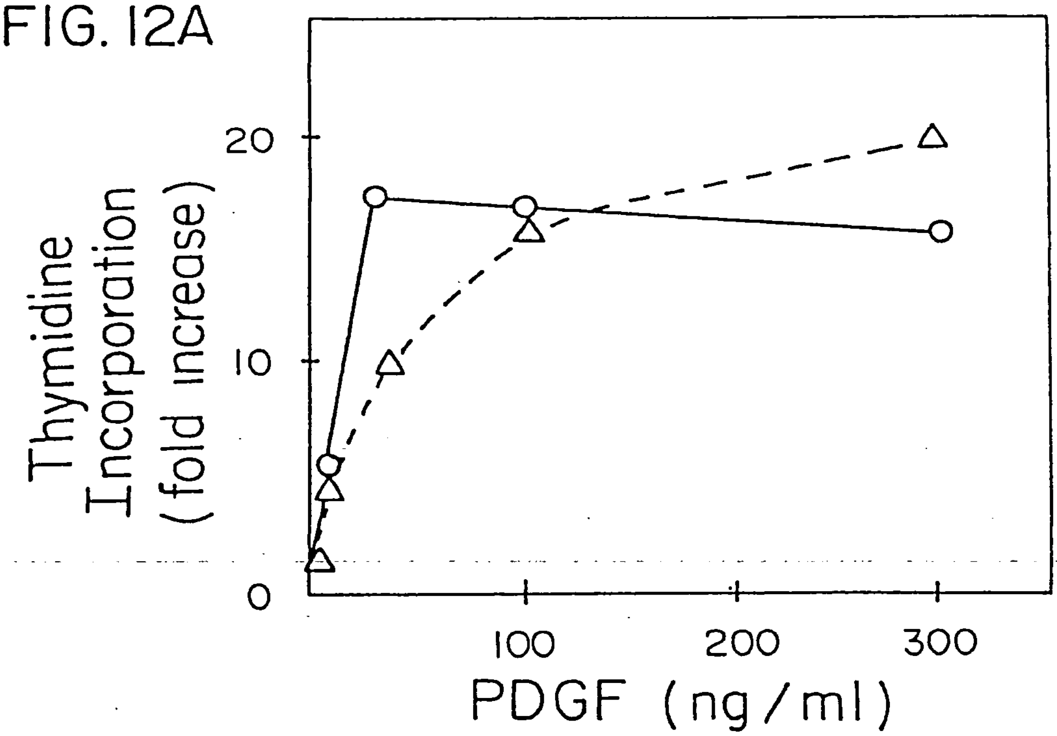


FIG. 12B

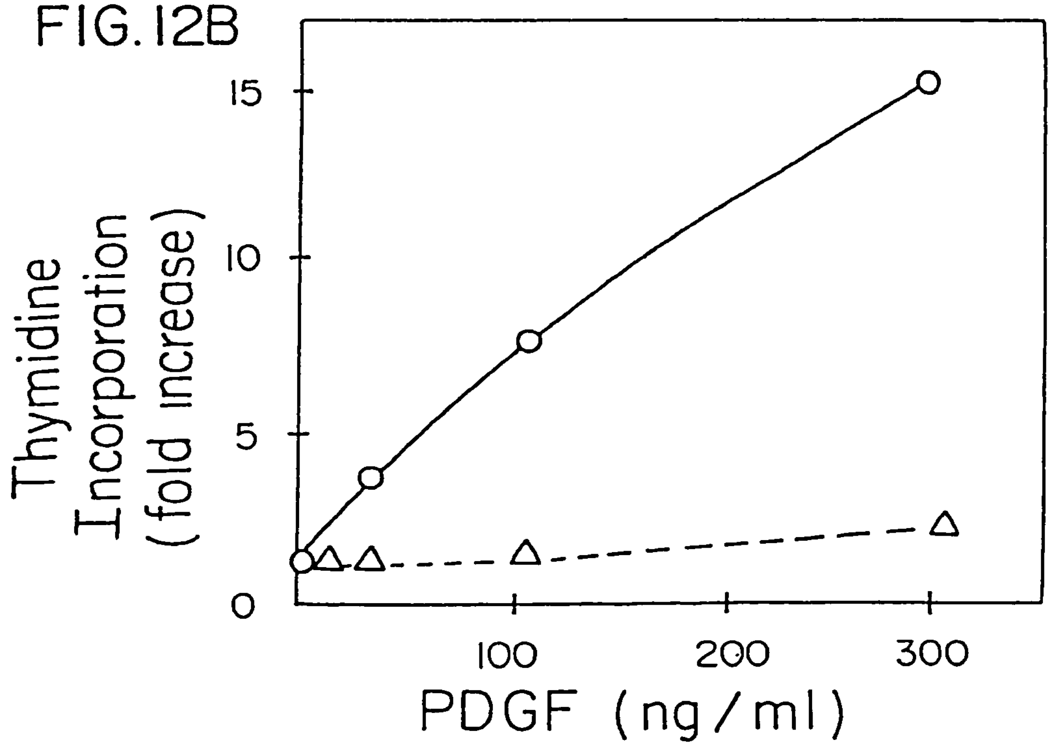


FIG. 13A

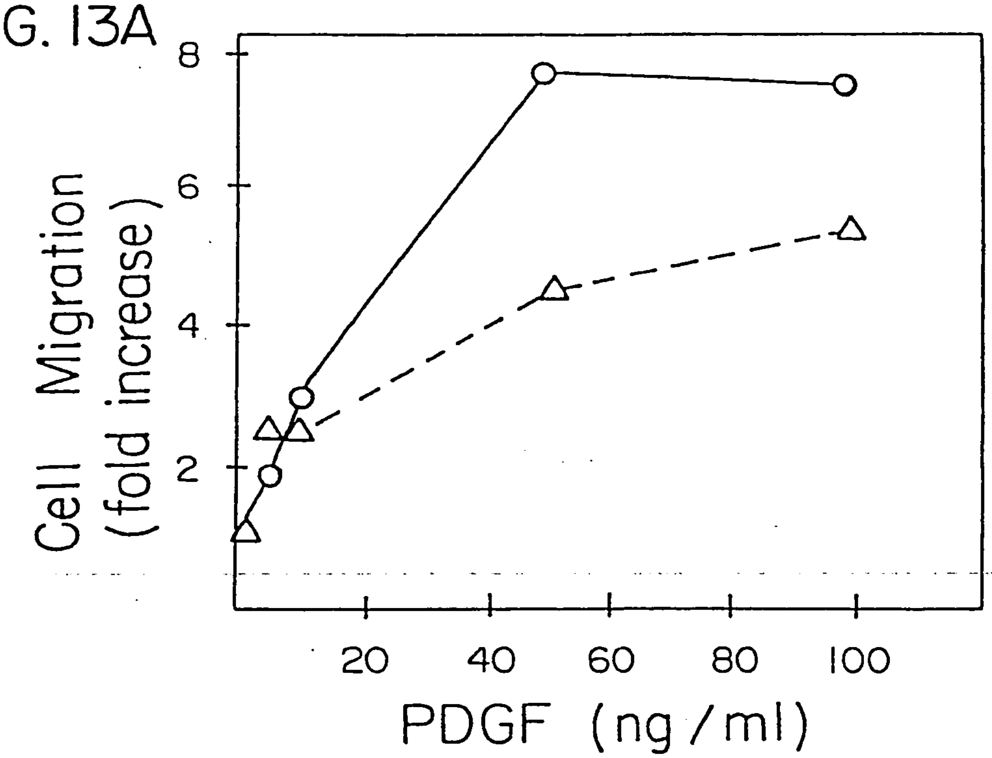


FIG. 13B

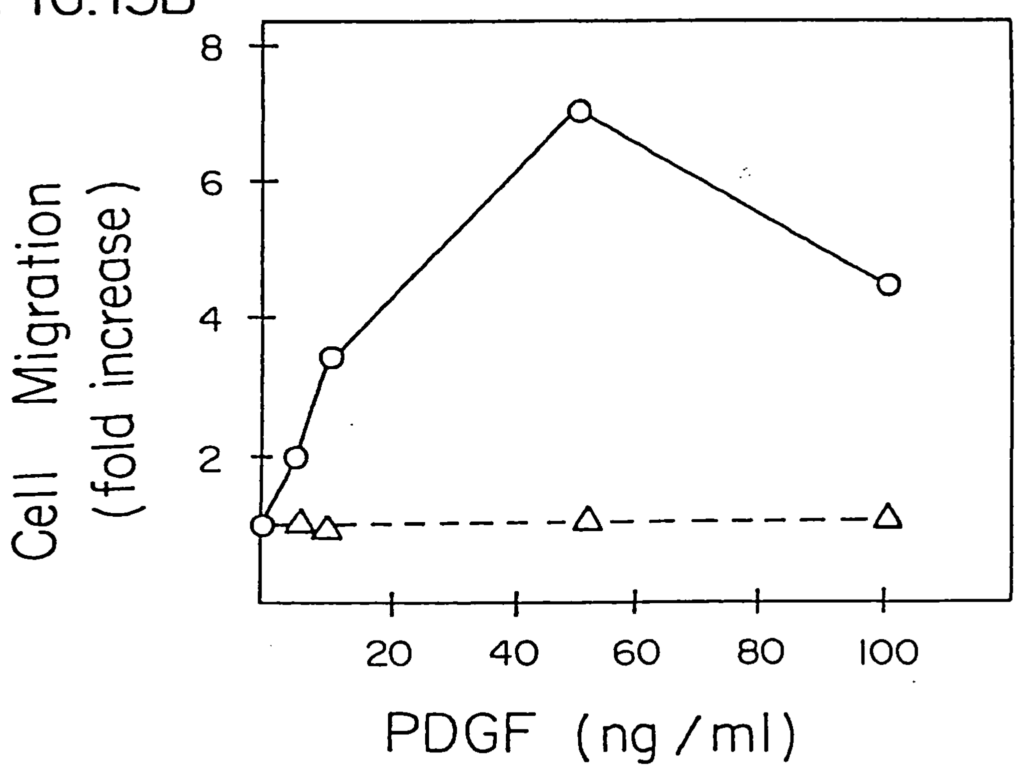


FIG. 14A

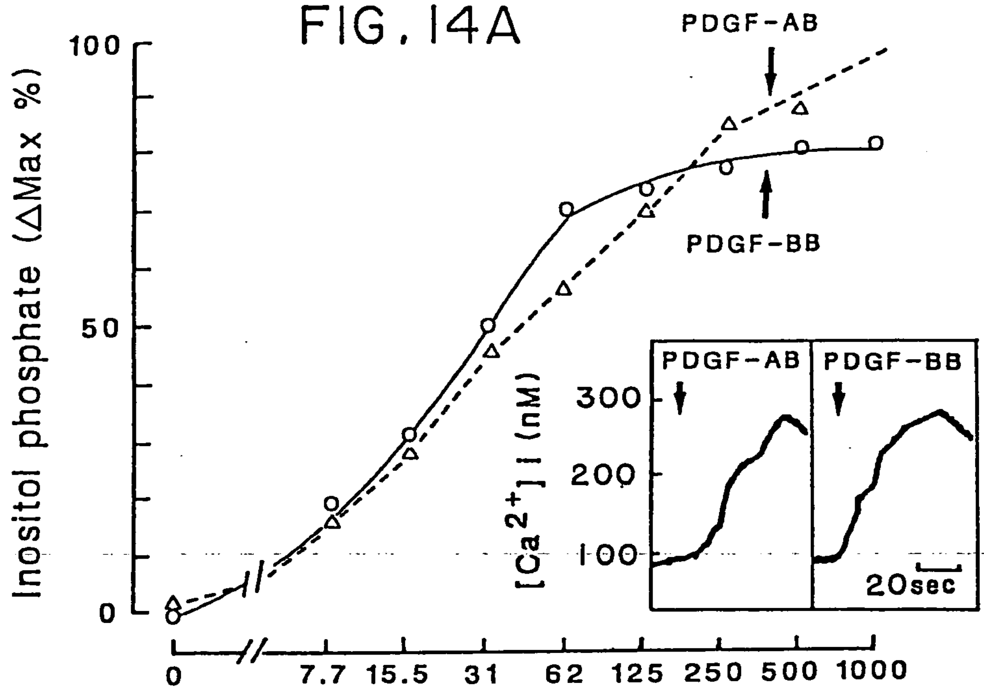


FIG. 14B